

89 22 8.6 7792 15 OCBCEBII O.cuniculus mRNA for b 1.29e+01
 90 22 8.6 7980 12 MXJ20669 Myxococcus xanthus rib 1.29e+01
 91 22 8.6 8608 15 OCBCEBII O.cuniculus mRNA for b 1.29e+01
 92 22 8.6 17286 21 HSRING H.sapiens gene encodin 1.29e+01
 93 22 8.6 34244 12 AORCZ363 Amycolatopsis orientai 1.29e+01
 94 22 8.6 38186 21 AC004449 Homo sapiens chromosom 1.29e+01
 95 22 8.6 41702 21 AC004156 Homo sapiens chromosom 1.29e+01
 96 22 8.6 47773 13 AC004189 *** SEQUENCING IN PROG 1.29e+01
 97 22 8.6 120630 12 MY025 Mycobacterium tubercu 1.29e+01
 98 22 8.6 135301 27 BHVIGEN Bovine herpesvirus 1 c 1.29e+01
 99 21 8.2 285 20 HUMHMRAC Human lymphocyte anti 3.99e+01
 100 21 8.2 1525 17 I05333 Sequence 11 from Paten 3.99e+01

ALIGNMENTS

RESULT 1 HUMERP 2304 bp mRNA PRI 13-DEC-1994
 LOCUS Human mRNA for estrogen responsive finger protein, complete cds.
 DEFINITION D1205
 ACCESSION 9458725
 NID estrogen responsive finger protein.
 KEYWORDS Homo sapiens placenta cDNA to mRNA, clone lambda C3.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2304)
 AUTHORS Inoue,S., Orlino,A., Hosoi,T., Kondo,S., Toyoshima,H., Kondo,T., Ikegami,A., Ouchi,Y., Orlino,H. and Muramatsu,M.
 TITLE Genomic blindng-site cloning reveals an estrogen-responsive gene that encodes a RING finger protein
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (23), 11117-11121 (1993)
 MEDLINE 94068555
 REFERENCE 2 (bases 1 to 2304)
 AUTHORS Inoue,S.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-1993) to the DDBJ/EMBL/Genbank databases. Satoshi Inoue, Faculty of Medicine, University of Tokyo, Department of Geriatrics, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113, Japan (E-mail:U01A1NO@PNUMIN.BITNET, Tel:03-3815-5411(ex.8344), Fax:03-5689-2483)
 COMMENT Submitted (18-Oct-1993) to DDBJ by:
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 Tokyo 113
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FEATURES

CDS

Location/Qualifiers
 1. 2304
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue-type="placenta"
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 /codon_start=1
 /product="estrogen responsive finger protein (efp)"
 /db_xref="pid:d1005279"
 /db_xref="pid:g458726"
 /translation="MAECPFLAEELSCICLPEPEPYTRPGHNCSCGCLNTMAVO GSPYCPORAYTOARPOLHKTIVLCNVEQFLQADLAREPADVTPPARASPSR AOVCDHCLKEAVATCVCNASCFCOEHLQPHFDPADPDPADVPDILRRCSOR NLRREFCESEHCICLYEHKTCSPASLSOASADLALRHKTVMYQINGASR ADDVNRQOVDMATNRKREVOLEQETEMKALDASSETSTRIKEREKVNSEFDT IYQILKKSEIOTLKEIEOSLITRDEFEFLERASKIRGISIPVPIPEVLNHLKI KGHSTIDIKNEIKELKOCIGROELTPSGGDEHPASTHSTPVKVSKEKSKR PPVPAISKPTPGAPOLVDLKOAGLEAAKATISSHPNSTSLKAVLEFLAKSR ELLEETIVILDTYTAHKKVALSECYTVAASVEMPONRPHPOFTYCSOVIGICHYK KIHWEVLEQKNFCGVGICYSNMNRQGPESRIGRNSASNCVEMFTKISANHNVE

BASE COUNT 544 a 673 c 659 g 428 t
 ORIGIN
 Query Match 16.8%; Score 43; DB 21; Length 2304;
 Best Local Similarity 59.8%; Pred No. 4,83e-12;
 Matches 122; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Db 64 GAGGAGCTGTCTGCTCATCTGCTGAGCGCTTCAAGAGCGCGTCACTCCGGT 123
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 18 GAGGAGCTCATCTGCTCATCTGCTGAGCGCTTCAAGAGCGCGTCACTCCGGT 77
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 124 GGCACACTTCTGCGGCTGCTGCTGATATAGACGTGGCGCATCCAGGCTCCCATAC 183
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 78 AAGCAGCTTCTGCGGCTGCTGCTGATGCGGCGCTGGCGCATCCAGGCGCTCGTA 137
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 184 CTGTGCGGCGAGTCCCGCGCTTACACGCGGCGGCGAGCTGCGACAGAACAGGTTG 243
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 QY 138 CGTGCGCGAGTGCACACAGGCTTACACAGAGCGGCGCTGGAGAGAACAGTGAAG 197
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 Db 244 CTGTGCAACGTGTGTGAGCAGTTTC 267
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 QY 198 CTCACCAACATCTGTGAGAGTTTC 221

RESULT 2
 LOCUS AC004584 103832 bp DNA HTG 10-JUN-1998
 DEFINITION *** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone hNPC1107_A_17; HTGS phase 1, 4 unordered pieces.
 ACCESSION AC004584
 NID 93209679
 KEYWORDS HTG: HTGS_PHASE1.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 103832)
 AUTHORS Birren,B., Fasman,K., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Human
 JOURNAL Submitted (17-APR-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html.

REFERENCE 2 (bases 1 to 103832)
 AUTHORS Birren,B., Fasman,K., McKernan,K., Nusbaum,C., Richardson,P., Lander,E., Allen,N., Baker,J., Baldwin,J., Barna,N., Beckert,R., Benn,J., Boatin,C., Boutwell,C., Brown,A., Byrne,S., Cantu,C., Castle,A., Cerny,J., Cooke,P., Daly,M.J., Depyre,E., Devon,K., Dewar,K., Donelan,L., Durette,B., Etemad,S., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Grant,G., Gray,D., Hagos,B., Harris,K., Houghton,L., Howland,J.C., Hul,L., Jacobot,L., Kann,L., Linton,L., MacDonald,P., Marguis,N., McMan,P., McGurk,A., Meldrum,U., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Nachman,A., Nahr,R., Naylor,J., O'Connor,T., Pavlin,B., Peterson,K., Riley,R., Roberts,D., Rollins,G., Rossello,R., Roy,A., Shyam,R., Stange-Thomann,N., Stillwell,J., Stone,K., Stickleland,C., Subramanian,H., Sydney,K., Tang,L., Torrella-Miller,I., Vasilleev,H., Vo,A., Wagner,A., Wang,B., Wheeler,J., Wu,Y., Ye,W.J., Zhao,J. and Zody,M.
 TITLE Direct Submission
 JOURNAL Submitted (17-APR-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html.

*** WARNING: Phase 1 High Throughput Genome Sequence ***
 *** This sequence is unfinished. It consists of 4 contigs for ***
 *** which the order is not known; their order in this record is ***
 *** arbitrary. In some cases, the exact lengths of the gaps ***
 *** between the contigs are also unknown; these gaps are presented ***
 *** as runs of N as a convenience only. When sequencing is complete, ***
 *** the sequence data presented in this record will be replaced ***